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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Tue Oct 23 10:26:56 EDT 2007

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Application No: 10594418 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2007-10-04 15:55:22.188  
**Finished:** 2007-10-04 15:55:24.040  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 852 ms  
**Total Warnings:** 27  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 27  
**Actual SeqID Count:** 27

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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
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**Input Set:**

**Output Set:**

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Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (22)
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# SEQUENCE LISTING

<110> Hexima Limited  
Poon, Simon  
Heath, Robyn L.  
Clarke, Adrienne E.

<120> Arabinogalactan Protein Compositions and Methods for Fostering  
Somatic Embryonic Competence

<130> 12639240/AJH

<140> 10594418

<141> 2007-10-04

<150> 60/558,609

<151> 2004-03-01

<160> 27

<170> PatentIn version 3.4

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tcttctgaat cagattctct caacaaatgg gctgaaaaag ctcgtttcca aatcggcgac      180

tctctcgtgt ggaaatatga tgggtggtaaa gactcgggtgc tccaagtgag taaggaggat      240

tatacaagtt gcaatacgtc gaacccgatt gccgagtaca aagatgggaa caccaagggtg      300

aagcttgaaa agtcaggacc atatttcttc atgagtggag caaagggccca ctgcgagcaa      360

ggccagaaga tgatttggtt tgtgatgtct caaaagcata ggtacattgg aatctctcca      420

gcaccttcgc cggttgattt tgaagggtccg gccgttgctc caacaagcgg agttgcaggg      480

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Phe Ile Phe Leu Ser Phe Ala Gln Gly Lys Glu Ile Met Val Gly Gly
      20              25              30

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Lys Thr Gly Ala Trp Lys Ile Pro Ser Ser Glu Ser Asp Ser Leu Asn
      35              40              45

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Lys Trp Ala Glu Lys Ala Arg Phe Gln Ile Gly Asp Ser Leu Val Trp
      50              55              60

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Lys Tyr Asp Gly Gly Lys Asp Ser Val Leu Gln Val Ser Lys Glu Asp
      65              70              75              80

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Tyr Thr Ser Cys Asn Thr Ser Asn Pro Ile Ala Glu Tyr Lys Asp Gly
      85              90              95

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Asn Thr Lys Val Lys Leu Glu Lys Ser Gly Pro Tyr Phe Phe Met Ser
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Gly Ala Lys Gly His Cys Glu Gln Gly Gln Lys Met Ile Val Val Val
      115              120              125

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Met Ser Gln Lys His Arg Tyr Ile Gly Ile Ser Pro Ala Pro Ser Pro  
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Val Asp Phe Glu Gly Pro Ala Val Ala Pro Thr Ser Gly Val Ala Gly  
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Leu Lys Ala Gly Leu Leu Val Thr Val Gly Val Leu Gly Leu Phe  
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gagaactaca atcattgggc tgaaaggaat agattccaag tcaatgatac tctctttttc 180  
aagtacaaga aagggtcaga ctcggtgctg ttggtaacaa gagaagatta cttctcatgc 240  
aacaccaaga acccaattca gtctttaaca gaaggtgatt cactctttac atttgatcgg 300  
tcgggtccct tctttttcat caccggtaac gctgataatt gcaaaaaagg gcaaaagctg 360  
atcgtcgtgg tcatggctgt aagacacaaa cccagcaac aacctccttc accttctccc 420  
tcatactgtg tgacaacagc gccggtttct ccaccacat taccattcc tgaaactaac 480  
cctcctgtag agtcaccaa gagcagtgag gctccatctc atgatgctgt ggaaccagct 540  
ccgccggagc acagatcggg ttcatcaaa ctagtatgtt ctacctggct ggtgttgggt 600  
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35 40 45

Arg Asn Arg Phe Gln Val Asn Asp Thr Leu Phe Phe Lys Tyr Lys Lys  
50 55 60

Gly Ser Asp Ser Val Leu Leu Val Thr Arg Glu Asp Tyr Phe Ser Cys  
65 70 75 80

Asn Thr Lys Asn Pro Ile Gln Ser Leu Thr Glu Gly Asp Ser Leu Phe  
85 90 95

Thr Phe Asp Arg Ser Gly Pro Phe Phe Phe Ile Thr Gly Asn Ala Asp  
100 105 110

Asn Cys Lys Lys Gly Gln Lys Leu Ile Val Val Val Met Ala Val Arg  
115 120 125

His Lys Pro Gln Gln Gln Pro Pro Ser Pro Ser Pro Ser Ser Ala Val  
130 135 140

Thr Thr Ala Pro Val Ser Pro Pro Thr Leu Pro Ile Pro Glu Thr Asn  
145 150 155 160

Pro Pro Val Glu Ser Pro Lys Ser Ser Glu Ala Pro Ser His Asp Ala  
165 170 175

Val Glu Pro Ala Pro Pro Glu His Arg Ser Gly Ser Phe Lys Leu Val  
180 185 190

Cys Ser Thr Trp Leu Val Leu Gly Phe Gly Ile Trp Val Ser Met Ala  
195 200 205

Leu Gly Ile Glu Asn Val Val Cys Phe Trp Cys  
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20 25 30

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35 40 45

Pro Ser Ser Glu Ser Asp Ser Leu Asn Lys Trp Ala Glu Lys Ala Arg  
50 55 60

Phe Gln Ile Gly Asp Ser Leu Val Trp Lys Tyr Asp Gly Gly Lys Asp  
65 70 75 80

Ser Val Leu Gln Val Ser Lys Glu Asp Tyr Thr Ser Cys Asn Thr Ser  
85 90 95

Asn Pro Ile Ala Glu Tyr Lys Asp Gly Asn Thr Lys Val Lys Leu Glu  
100 105 110

Lys Ser Gly Pro Tyr Phe Phe Met Ser Gly Ala Lys Gly His Cys Glu  
115 120 125

Gln Gly Arg Lys Met Ile Val Val Val Met Ser Gln Lys His Arg Tyr  
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Ile Gly Ile  
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Gly Ser Tyr Lys Phe Tyr Val Gly Gly Arg Asp Gly Trp Val Val Ser  
35 40 45

Pro Ser Glu Asn Tyr Asn His Trp Ala Glu Arg Asn Arg Phe Gln Val  
50 55 60

Asn Asp Thr Leu Phe Phe Lys Tyr Lys Lys Gly Ser Asp Ser Val Leu  
65 70 75 80

Leu Val Thr Arg Glu Asp Tyr Phe Ser Cys Asn Thr Lys Asn Pro Ile  
85 90 95

Gln Ser Leu Thr Glu Gly Asp Ser Leu Phe Thr Phe Asp Arg Ser Gly  
100 105 110

Pro Phe Phe Phe Ile Thr Gly Asn Ala Asp Asn Cys Lys Lys Gly Gln  
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